

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 16, 2005, 16:16:11 ; Search time 38.2706 Seconds  
(without alignments)  
2330.594 Million cell updates/sec

Title: US-10-003-356-8

Perfect score: 4904

Sequence: 1 MFERRKEQDEGPGCIHEFLAF.....TVSTVLDDRVLYMCPLKIQ 927

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695.5	34.6	1085	2 S40476	Ca(2+)-sensing rec
2	1690.5	34.5	1079	2 I59362	calcium/polyvalent
3	1687.5	34.4	1078	2 A56715	calcium receptor (
4	1673.5	34.1	1088	2 B56715	calcium receptor (
5	845	17.2	858	2 JC7683	taste receptor TIR
6	835.5	17.0	879	2 JC7160	metabotropic gluta
7	821.5	16.8	1218	2 S71376	glutamate receptor
8	814.5	16.6	879	2 JH0562	metabotropic gluta
9	795.5	16.2	1180	2 JC2132	metabotropic gluta
10	795.5	16.2	1212	2 JC2131	metabotropic gluta
11	794	16.2	1199	2 A41939	G protein-coupled
12	776	15.8	1171	2 A42316	metabotropic gluta
13	764	15.6	872	2 JH0561	metabotropic gluta
14	758	15.5	915	2 A49874	metabotropic gluta
15	724.5	14.8	871	2 A46742	metabotropic gluta
16	707.5	14.4	912	2 JH0563	metabotropic gluta
17	691.5	14.1	1267	2 T21340	hypothetical prote
18	679	13.8	908	2 I49142	metabotropic gluta
19	656	13.4	999	2 T27628	hypothetical prote
20	398	8.1	551	2 T30806	metabotropic gluta
21	296	6.0	1099	2 T16283	hypothetical prote
22	215	4.4	923	2 T51136	ionotropic gluta
23	211	4.3	923	2 F84732	probable ligand-ga
24	194	4.0	997	2 S33754	glutamate receptor
25	188	3.8	933	2 C96495	probable ligand-ga
26	185.5	3.8	1039	2 T45779	probable glutamate
27	168.5	3.4	953	2 E84732	probable ligand-ga
28	163	3.3	960	2 JEO356	gamma-aminobutyric
29	157	3.2	950	2 T51134	ionotropic gluta

30	156.5	3.2	976	2 T51137	ionotropic gluta
31	150	3.1	962	2 D86186	hypothetical prote
32	149.5	3.0	934	2 T02742	probable ligand-ga
33	149.5	3.0	941	2 T51135	ligand-gated chann
34	149	3.0	912	2 T51131	ligand gated chann
35	138.5	2.8	925	2 T51133	ligand gated chann
36	138.5	2.8	951	2 T51132	probable glutamate
37	138.5	2.8	958	2 T02741	probable ligand-ga
38	138.5	2.8	975	2 A84550	probable ligand-ga
39	134	2.7	925	2 T06128	hypothetical prote
40	129	2.6	824	2 T51057	related to tol pro
41	129	2.5	943	2 A47551	N-methyl-D-asparta
42	125	2.5	354	2 T33395	hypothetical prote
43	124	2.5	906	2 JNO341	N-methyl-D-asparta
44	124	2.5	922	2 JNO340	N-methyl-D-asparta
45	124	2.5	959	2 JNO336	N-methyl-D-asparta

ALIGNMENTS

RESULT 1

S40476

Ca(2+)-sensing receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S40476

R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifer, O.; Sun, A.;

Nature 366, 575-580, 1993

A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from

A:Reference number: S40476; MUID:94077182; PMID:8255296

A:Accession: S40476

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1085 <BRO>

A:Cross-references: UNIPROT:P35384; GB:S67307; NID:G453108; PIDN:AAB29171.1; PID:G45310

Query Match 34.6%; Score 1695.5; DB 2; Length 1085;  
Best Local Similarity 39.3%; Pred. No. 3.8e-116;  
Matches 350; Conservative 173; Mismatches 323; Indels 45; Gaps 15;

QY	53	LVIGLFPIDSRITIPANESI-LEPASAKCEGNFORFRMKAMIMIKINRKOILPNI	111
DB	33	IILGLFPFHGAVAKDQLSRPSEVICIRYFRGRWLQAMIFAIEBINSSPALLPNN	92
QY	112	TLGYOIEDTCFTTISKVEAVLVFLTCQE---ENRPNFRNSTGAPPA--GIVGAGGSFLSV	166
DB	93	TLGYRIFDTCNTVSKALEATLSFVAQNKIDSLNLDFFCNCSEHIPSTIAVVGATGSGIST	152
QY	167	PASRILGLYLPQGVGTSTCVILSDKYQPPSYLRVIASDKIQSKAVVKRIQHFGWVWGA	226
DB	153	AVANLLGLFYIIPQVSYASSRLLSNKNQPKSFLRTIPNDEHQATAMADIIEYFRWNVGT	212
QY	227	IAADDYGYKVTKPKRMESANLCVASETTPKVYSNEMQKAVKAVTSTAKVILVYT	286
DB	213	IAADDYGRPGTEKFEFEAEERDICTDFSELISQYSDERKIQQWVEVIQNSTAKVIVFSL	272
QY	287	SDIDLSLFVLEMHNIHNTDRTWIAETATSALIAKPEVFPYFGGTIGFATPRSVPLGLK	346
DB	273	SGFDLEPLIKELVRRNITGRILWASEAWASSLLIAMPFYHVVGTTIGFGLKAGQIPGPR	332
QY	347	EFLYDVHPNKPNDVLTITFMQTAFNC-TWPNSSVPYVNDVHRVNMVTKEDRLYDMSDQ--	403
DB	333	EFLQKVHPKSVHNGFAKEFWETFNCHLOEAKGKPLPVD--TFLRGHEGGARLNSPT	390
QY	404	----LCTGSEKLEDKNTYLDTSQLRITKQCKQAOVAYIAHGLDHLSCQEGQPGFSGNQ	459
DB	391	AFRPLCTGENTSSVETPMYDTHLRISVNVYLAIVVIAHALQDIYTCIPGRGLF-TNGS	449
QY	460	CAYITFDVQWLYMYKEIKPKSHEDKWLIDNDGDKNGHYDVLNHLWD-DEGEISFTV	518
DB	450	CADIKKVEAWQVLRHLRHLNFTSNMGEQVTFDECGDLA-GNYSIINHLHSPEDGSIVFKE	508

QY 519 VGRFNRFRNFIIVLTPTNSTIIFWNTSSRRSLPHSVCTDVCPPGTGRTGFVQRPEIPCCFDSP 578  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 509 VGYNVYAKGBRLFINDEKILMGSGFSREVFPNSCRDLAGTRKGIIIEGEBTCCFECEV 568  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 579 CADGHVSRRPGERECEQCEDYWSNAOKSECVLKEVEVLAYDEALGFVLTLISLVFGAFVV 638  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 569 CPDGEVDTEFASACKCPDPFWSENHTSCIAKIEFLSWTEPGIALTLFNVLGIFLT 628  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 639 LAVTAVYVIRHRTLPLVNADWDGLFLIQVLSLIIMLLSNMLFIDKPNNWSCMAGQTTLAIG 698  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 629 AFVLGVFIKRNTPVKATNRELVSILLFLLSCCFSSSFFFIGEPQDWTCRLRPAFGIS 688  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 699 FSLCLSLGLKGTSSLFLAYRISKTKOLTSMHPYRK-----IIVLISVLAEIGICT 750  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 689 FVLICISILVKNRVLLVF--EAKIP-TSFH---RKMWLMQLQFLVLCFTFMQIVICA 741  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 751 AVYLILPPMVYKNMESQNTKIILGCNEISIBELYSNFGIDAFIALLCFLTTFVARQLPDN 810  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 742 IWLNTAPPSYRNHELEDEIIPITCHEGSLMALGFLGYTCLLAACIFFFAFKSRKLLEN 801  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 811 YYEGKCITGMLVPFIINMSFVPVYLVSTVGKFMVAIVEIPAILASHGLLGICIFAPKCLII 870  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 802 FNEAKTITTSMLIFFTVWISFIPAVASTYTGKFSVAVEVIALLASFGLLACIFFNKVYII 861  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 871 LLAPERNTSIIVCGRYSTTDNCILTSAFV-----SSELNNTTVST 911  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 862 LFRPSRNTIEV--RCSTAHAFKVAARLATLRNSVRSORSSSLGGSTGST 910  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
  
RESULT 2  
159362  
calcium/polyvalent cation-sensing receptor precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I59362; A55594  
R;Ruut, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.  
Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995  
A;Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve te  
A;Reference number: I59362; MUID:95241465; PMID:7724534  
A;Accession: I59362  
A;Status: translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1079 <RES>  
A;Cross-references: UNIPROT:P48442; EMBL:U20289; NID:g790578; PIDN:AAC52195.1; PID:g7905  
R;Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995  
A;Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval  
A;Reference number: A55594; MUID:95116508; PMID:7816802  
A;Accession: A55594  
A;Molecule type: mRNA  
A;Residues: 1-133 'X', 135-1079 <RIC>  
A;Cross-references: GB:U10354  
A;Experimental source: kidney  
C;Keywords: calcium; glycoprotein; phosphoprotein; transmembrane protein  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;187-212/Region: hydrophobic  
F;613-635/Domain: transmembrane #status predicted <TM1>  
F;650-670/Domain: transmembrane #status predicted <TM2>  
F;683-700/Domain: transmembrane #status predicted <TM3>  
F;725-744/Domain: transmembrane #status predicted <TM4>  
F;770-790/Domain: transmembrane #status predicted <TM5>  
F;806-828/Domain: transmembrane #status predicted <TM6>  
F;841-860/Domain: transmembrane #status predicted <TM7>  
F;90-261,287,396,468,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #statu  
F;794/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict  
  
Query Match 34.5%; Score 1690.5; DB 2; Length 1079;  
Best Local Similarity 38.0%; Pred. No. 8.7e-116;  
Matches 352; Conservative 181; Mismatches 332; Indels 61; Gaps 17;  
  
OV 18 LAFLW--AELGSEAKEEKKEERTCKLLGCKVDENSHSLVIGGLPFIDRSRTIPANESI-LE 74

A:Reference number: A56715; MUID:95279439; PMID:7759551  
A:Accession: A56715  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1078 <GAR>  
A:Cross-references: GB:U20759; NID:9683744; PIDN:AAA86503.1; PID:9683745  
R:Pearce, S.H.S.; Thakker, R.V.  
submitted to the EMBL Data Library, August 1994  
A:Reference number: S49341  
A:Accession: S49341  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>  
A:Cross-references: EMBL:X81086  
R:Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,  
Cell 75, 1297-1303, 1993  
A:Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric  
A:Reference number: A49419; MUID:94094324; PMID:7916660  
A:Accession: A49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 178-192 <POL>  
A:Experimental source: family N  
A>Note: sequence inconsistent with nucleotide translation  
A>Note: sequence modified after extraction from NCBI backbone  
A>Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and ne  
A>Note: sequence extracted from NCBI backbone (NCBIN:142453)  
A:Accession: B49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 289-303 <PO2>  
A:Experimental source: family E  
A>Note: sequence modified after extraction from NCBI backbone  
A>Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and ne  
A>Note: sequence extracted from NCBI backbone (NCBIN:142455)  
A:Accession: C49419  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 788-802 <PO3>  
A:Experimental source: family J  
A>Note: sequence modified after extraction from NCBI backbone  
A>Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and ne  
A>Note: sequence extracted from NCBI backbone (NCBIN:142457)  
A:Keywords: glycoprotein; receptor; transmembrane protein

Query Match 34.4%; Score 1687.5; DB 2; Length 1078;  
Best Local Similarity 38.0%; Pred. No. 1.5e-115;  
Matches 353; Conservative 179; Mismatches 333; Indels 63; Gaps 18;

QY 18 LALFW--AELGSEAKEKEEBERTCRLGKCVDAENHSLVIGGLPPTDSRTIPANESI-LE 74  
DB 11 LALTWHTSAYGPDQRAQKGD-----IILGGLPFIHFVGAQDQDLKSR 54  
QY 75 PASACEGNFQFRFMKAMIMIKENKRDILPNTILGYQIFDTCFTISKSVEALVLF 134  
DB 55 PESVEICIRYFRGFWLQAMIFAEEINSPALLPNTILGYRIFDTCNTVSKALEATLSF 114  
QY 135 LTQGE---ENRPNFNSTGAPFA--GIVGAGGSFLSVPASRILGLYLPOVGYTSCVIL 189  
DB 115 VAQNKIDSLNDFECNCSHPISTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLL 174  
QY 190 SDKYQPPSLRVIASDKIQSKAVKRIQHFQVWVWGAATAADDYGYGVKTFKEMESAN 249  
DB 175 SNKNQPKSLRTIPNDEHQATAMADIIIEYFRNWNVTIAADDYGRPGIEKFEAREERD 234  
QY 250 LCVAFSETIPKIVSNKQAKAVKATSTAKVILVYTSIDLSLVLEMIHNTDRTWI 309  
DB 235 ICIDFSELISQYSDBEIQHWVEVIQNSTAKVIVFSSGPDLEPLIKVIRRNITGKIWL 294  
QY 310 ATEANITSLIAKPEYFPFGCTIGPATPSRIVGLKEELYDVHNPKNPDNDVLTIEFWQT 369  
DB 295 ASEAWASSLIAMPOYFHVVGTTIGTGFALKAGQIQGREFLKKVHPKRSVHNGFAKEFWEE 354

QY 370 AFNC-TWPNSSVPYVNDHRVNMVTKGE---DRLYDMSD---QLCTGEEKLEDLKNYTLDTLS 422  
DB 355 TFNCHLQEGAGLPVD--TFILRGHEBSGDRFSNSTAFRPLCTGDENISSVETPIDYT 412  
QY 423 QLRITKQCKQAVYAIAGHLDHLSRCQBGQPPGSGNQCCAYIPTDFWQLMYMKIIFKFS 482  
DB 413 HLRISSYNVYLAIVSYIAHALQDIYTCPLGRGLF-TNGSCADIKKVEAWQVILKHLRLHNFN 471  
QY 483 HEDKWVILDDNGDLKNGHVDVNLNHL-DGEGISFVTVGRENFRSTNPELVIPNTSTIFW 541  
DB 472 NNGEQVTFDECGDLV-GNYSIINHLSPEDSIVFKEVYNNVYAKGERLFINKEKILM 530  
QY 542 NTESSLPHSVCTDVCPEGTGQGFQVREPICCFDSIPCADGHVSRKPGERECEQCGEDYW 601  
DB 531 SGFSREVFPFNSCRDCLAGTRKGIIEGSEPTCCFECEVCPDGEYSDETASACNKCPCDDFW 590  
QY 602 SNAQXSECVLKEVEVLAYDEALGFTLVILSVFGAPVLAIVYVHRTPLVNASDWQL 661  
DB 591 SNEHNTSCIAKEIEFLSWTEPFGIALTLFVLGIFLTAFLVGLVFIFKFRNTPIVKATNREL 650  
QY 662 GFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFLSLCLSLGKTSLSFLAYRISK 721  
DB 651 SYLLLFSLCCFSSSLFFIGEPQDWTCLRQAPAGISFVLCSILVKTNRVLLVF--B 707  
QY 722 SKTQLTSMHPLYRK-----IIVLISVLABIGICTAYLILEPPPMYKNMESQNTKIL 773  
DB 708 AKIP-TSPH---RKWGLNLQFLVFLCTFMQIVICVILVLTAPPSSYRNQBLEDEIIFI 763  
QY 774 GCNEISIEFLYSMFGIDAFIALLCLPTTFVARQLPDNYVEGKCIITFGMLVPIIWMSPVP 833  
DB 764 TCEGSLMALGFLIGYTCLLAAICFPFAPKSRKLPENFNFAKPIITFSMLPIFVWISFIP 823  
QY 834 VYLSKTKGFKMAVEIFAILASSHGLGCIAPKAPKLIILLRPERNTSEIVCGVSTTDNCI 893  
DB 824 AYASTYGFSAVEVIALAASFGLLACIFPNKIYIILFKSRNTIEV--RCSTAAHAF 881  
QY 894 QLTSAFV-----SSHLNNTTVST 911  
DB 882 KVAARATLRNSVSRKRSLSLGGSTG 909

RESULT 4  
B56715  
calcium receptor (clone pHpCa-5.2) - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C:Accession: B56715  
R:Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.  
J. Biol. Chem. 270, 12919-12925, 1995  
A:Title: Molecular cloning and functional expression of human parathyroid calcium receptor  
A:Reference number: A56715; MUID:95279439; PMID:7759551  
A:Accession: B56715  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1088 <GAR>  
A:Cross-references: GB:U20760; NID:9683746; PIDN:AAA86504.1; PID:9683747  
C:Keywords: glycoprotein; receptor; transmembrane protein

Query Match 34.1%; Score 1673.5; DB 2; Length 1088;  
Best Local Similarity 37.6%; Pred. No. 1.6e-114;  
Matches 353; Conservative 180; Mismatches 332; Indels 73; Gaps 19;

QY 18 LALFW--AELGSEAKEKEEBERTCRLGKCVDAENHSLVIGGLPPTDSRTIPANESI-LE 74  
DB 11 LALTWHTSAYGPDQRAQKGD-----IILGGLPFIHFVGAQDQDLKSR 54  
QY 75 PASACEGNFQFRFMKAMIMIKENKRDILPNTILGYQIFDTCFTISKSVEALVLF 134  
DB 55 PESVEICIRYFRGFWLQAMIFAEEINSPALLPNTILGYRIFDTCNTVSKALEATLSF 114  
QY 135 LTQGE---ENRPNFNSTGAPFA--GIVGAGGSFLSVPASRILGLYLPOVGYTSCVIL 189  
DB 115 VAQNKIDSLNDFECNCSHPISTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLL 174

C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: transmembrane protein

Query Match	17.2%	Score 845;	DB 2;	Length 858;
Best Local Similarity	28.0%;	Pred. No. 8.8e-54;		
Matches 238;	Conservative 164;	Mismatches 382;	Indels 66;	Gaps 23;

  

Qy	54	VIGGLPFDISRTTPANESILEPASACEGFNFQRFMMKAMHMIKEINKRKDILPNITL	113
Db	36	ILGGLFLPGSTEBATLNQRTQPNISIPCNRFSLPLGLFLAMAMKMAVEINNGSALLPGLRL	95
Qy	114	GYOIFDTCTTISKSVAEVLFTG--QEENRPFNRSTGAFP--AGIVGAGGSFLSPASR	170
Db	96	GYDLFTCTSEPVVTKSSLMFLAKVGSQSIAYCNTQYQPRVLAVIGHSHSELALITGK	155
Qy	171	ILGLYLPQGVYTSCTVILSKYQPSYLURVIAASKIQSAKVVKRIQHFQGWVWGIAAD	230
Db	156	FFSFFLMPQVSASMDRLSDRETFSPFTVPSDRVOLQAVVLTLLQNFSSNNVAAALGSD	215
Qy	231	DDYKGYGVKTEKEMESANLCVAFSETIPKVSYN-----EKMQKAVKAVTSTAKVILVT	286
Db	216	DDYGRGLSTFISLANARIGICIAHEGLVPHQDTSQQLGKGLVDLTVQNVQSKVQVVVLEA	275
Qy	287	SDIDLFLVLEHMHNITDRTWIAEAWTTSALIAKPEYFFFGTIGTIGPATSPRSVIPGLK	346
Db	276	SARAVYSLSYSIIHGSLSPKVVAVSESMLTSLDVMTLPNIARVGTVLGLQRGALLP---	332
Qy	347	EFLYDVHPN-----KDPNDVLITTFQQTAPNCTWPNSSVPYNVDHVRNMTGKEDRLYD--M	400
Db	333	EFSHYVETHLAADP-----AF-C-----ASLNAELDLBEHVMGQRCPRCDDIM	376
Qy	401	SDQLCTGEEKLDELKNTYLDTSQLRITTKQKQAVYAIAGHLHLSRCEQGGPFGSGNOQC	460
Db	377	LQNLSSG--LLQNLSSAGQLH-HQIPAT---YAAVYSVAQALHNTLQCNVSHCHVSEH---	427
Qy	461	AYIPTFDFQLMYYMKEIKPKSHEDKXVILDDNGDLKNGHYDVLANHLLDDEGEISFVTVG	520
Db	428	-VLP-----WQLLENMYNMSFHA-RDLTLQFDAQGNV-DMEYDLKMWVMQSPTEV-LHTVG	479
Qy	521	RNFNRSTNPELVIPNTNSTITFNWTESSRLSPHSVCTDVCPPGTGR---GFVQREPICCFDSI	577
Db	480	TFN---GTQLQ---QQSKMYW--PGNQVPVSQCSQCKDQGVRRVKGFSH---CYDCV	527
Qy	578	PCADGHVSRKPGERECEQGDYWSNAQSECVLKEVYLAYDEALGFTVLTVLSVFGAFV	637
Db	528	CKKAGSYRKHPDFTCTPCNQDQWSPKSTACLPRPKPFLAWGEPVWLSLLLLCLVLGL	587
Qy	638	VLAATVAVVYHRRTPLVNASDWQLGFLVQSLIIMLSSMLFIDKPHNWSCHAGQVTAL	697
Db	588	ALAAALGSLVHWDSPFLVQASGGSCFGICLGLFCLSVLLFPGRPSASCLAAQOPMAHL	647
Qy	698	GFSLCSCLLGKTSLSFLAYR--ISKSTQLTSMHPLYRKIIIVLSLAEIGICTAYILIT	755
Db	648	PLTGCLSTLFLQAATFEVESELPFLSWANWLCSYLRGLWALVLLATFVEAALCAWYLIA	707
Qy	756	EPNMYVKWMSQNTKIILGCNEISIEFLYSMHGIDAFIALICFLTTFVARQLPDNYYEGK	815
Db	708	FPEPVVTDWSVLPTEVLEHCHVRVSVSLGLVHITNAMLAFICFLGTFTFVQSQPGRYNAR	767
Qy	816	CITFGMLVFFITWMSFVPVWLSGTGKFKMAVEIFAILLASSHGLLCIEFAPKCLIIILLRPE	875
Db	768	GUTFAMLAYFITWVSFVPLLNVQVAYQAVQMGAALLVCALGILVTFHLPKCYVLLWLPK	827
Qy	876	RNTSEIVGR	885
Db	828	LNTQBFLLGR	837

RESULT 6  
JC7160  
metabotropic glutamate receptor subtype 3 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Mar-2000 #sequence revision 04-Mar-2000 #text change 11-May-2000

RESULT 6  
JC7160  
metabotropic glutamate receptor subtype 3 precursor - mouse  
CjSpecies: Mus musculus (house mouse)  
CjDate: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000

C;Accession: JC7160  
R;Minoishi, T.; Nakanishi, S.  
J. Biochem. 126, 889-896, 1999  
A;Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3  
A;Reference number: JC7160; MUID:20012997; PMID:10544282  
A;Accession: JC7160  
A;Molecule type: DNA  
A;Residues: 1-879 <MIN>  
A;Cross-references: GB:AF170696  
C;Genetics:  
A;Gene: mGluR3  
C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <NAT>  
F;577-599/Domain: transmembrane #status predicted <TM1>  
F;614-634/Domain: transmembrane #status predicted <TM2>  
F;646-664/Domain: transmembrane #status predicted <TM3>  
F;689-709/Domain: transmembrane #status predicted <TM4>  
F;735-756/Domain: transmembrane #status predicted <TM5>  
F;770-791/Domain: transmembrane #status predicted <TM6>  
F;804-828/Domain: transmembrane #status predicted <TM7>  
  
Query Match 17.0%; Score 835.5; DB 2; Length 879;  
Best Local Similarity 26.8%; Pred. No. 4.5e-53;  
Matches 242; Conservative 167; Mismatches 389; Indels 105; Gaps 31;  
  
QY 53 LVIGGLPIDSRTIPANESILEPASAKCEGFNQR-FRWKAMIHMIKEINKEKIDLPNI 111  
DB 39 LVIGGLPINEKGTGTEE-----CRGINDRGIQRLEAMLPALDEINKDNKYNLLPGV 89  
  
QY 112 TLGYQIPDTC-----FTISKSVAVLPLTQSENRNFRNSTGAPP-----AGIVG 158  
DB 90 KLGWHILDTCSRDTYALEQSLFVRASLTQVDS-ABVMCPDGSVAIQENIPLLIAGVIG 147  
  
QY 159 AGSFSLVSPASRILGLYLLPQVGYTSTCVILSKYQFPSPVLRVIADSKVQKAVKRIQH 218  
DB 148 GSYSSVSIOQANLLRLFIQIPQISYASTSAKLSKRSYDYPARTVPPDFYQAKAMAILRY 207  
  
QY 219 FGWVWGAIAADDYGYKGVKTPKEMESANLCAVAFSETIPKYSNEKQKAVK-AVKTS 277  
DB 208 FNTYVSTVASEGDYGETGEAEQEARLNICIAEAKVGRNIRKSDVSIRELLQKP 267  
  
QY 278 TAKVILVYTSIDLSLFLVLEMIHNITDRTWIATFAWITSALIAK-PEYFPYFGGTIGFA 336  
DB 268 NARVVLFWESDDRELIAASRVN-ASFTWVASDCWGAQESIVKGSSEHAY--GAITLE 324  
  
QY 337 TPASVPLGKFLYDVHPNKPNDVLTIEFWQAFNCTWPNSSVPYVNDHVNMTGKDR 396  
DB 325 LASHPRVQRDYFQSLNPNYNNHNPFRDPFWEQKFCQSLQNK------NHR----- 370  
  
QY 397 LYDMSDOLCTGEEKLEDKNTYLDTSQRLITKCKQAVVAIAHGLDLSR--COEQGGPP 454  
DB 371 -----QIC--DKHLAIDSNYSQESKIMFV-----VNAVAMAHLMQMORTLCP----- 413  
  
QY 455 GSNQQAQYIPTDFWQLMY-YMKEIKF-----KSHEDKWVILDDNGDLKNGHYDVLNW- 506  
DB 414 NTTKLCDAKMLDGLKLYDKYLLKINFAPPNPKGADSVKEDTYGD-GMGRYNVFNQ 472  
  
QY 507 HLDDEGEISFVTVGRNFRSTNPELVIPNTSTIIFWNTESRLPHSVCTDVPFGTGRGVF 566  
DB 473 HIG--GKYSYLKGVHW-----AETLYLDVDSIHWSRNS--VPTSCSDPCAPENMKM-M 521  
  
QY 567 QREPICFDSIPCADGHVSRKP-----GERECQCGEDYWSNAQKSECVLKEVEYLAYDE 621  
DB 522 QPDVCCWICIPC-----EPYEYLVDEFTCMDCGPGQMPADLGCYNLPEDYIRWED 574  
  
QY 622 ALGFTLVILSVFGAVVAVTAVYVIRHRTPLVNASDQWQLGFIQVLSIIMLSSMLFID 681  
DB 575 AWAIGPTVIACLFMCTCIVITFIKHNNTPLVAKSGRELICYILLFGVSLSYCMTFFFA 634  
  
QY 682 KPNWNSCMAQVTLALGFSICLSGLLKTSSFLAYRISKTKQLTS-MHPLVRKIIVLI 740

DB 635 KPSPVICALRRRLGLGTSFAICYSALLTKTNCIARIIDGKVGNAQRPKFISPSQVFCIG 694  
QY 741 SVLABIGICTAYLILEPPMV--YKNMESQNTKIILGCNEISIEFLYSMEGIDAFALLCF 798  
DB 695 LILVQIVMVSVMLLETPTGTRYTLPEKRET-VILKCNVYKDSMLISL-TYDVLVLICT 752  
QY 799 LTTTFVARQLPDNYEGKCIITFGMLVFPFIIMWSFVPVYLSKQKFKMAVIFAILASSHG- 857  
DB 753 VYAFKTRKCPENFEAKFPGFTMYTTCIILWLAFLPIFYVTSSDYRVQTTMTCISVLSGF 812  
QY 858 -LLGCIIPAPKCLIIILRPENITSEIVCGRVSTTDNCIQLTSAPVSELNNTTVTVLDDR 916  
DB 813 VVIGCLFAPKVIHLVLPQKN---VVTHRLHLNRFVSVGTATYTSQSSASTYVPTVCNGR 869  
QY 917 VLI 919  
DB 870 EVL 872  
  
RESULT 7  
S71376  
glutamate receptor homolog - cherry salmon  
C;Species: Oncorhynchus masou (cherry salmon)  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 09-Jul-2004  
C;Accession: S71376  
R;Kubokawa, K.; Miyashita, T.; Nagasawa, H.; Kubo, Y.  
FEBS Lett. 392, 71-76, 1996  
A;Title: Cloning and characterization of a bifunctional metabotropic receptor activated  
A;Reference number: S71376; MUID:96354880; PMID:8769318  
A;Accession: S71376  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-1218 <KUB>  
A;Cross-references: UNIPROT:Q902F3  
C;Keywords: glycoprotein; phosphoprotein  
F;603-625/Domain: transmembrane #status predicted <TM1>  
F;640-660/Domain: transmembrane #status predicted <TM2>  
F;672-690/Domain: transmembrane #status predicted <TM3>  
F;717-737/Domain: transmembrane #status predicted <TM4>  
F;761-782/Domain: transmembrane #status predicted <TM5>  
F;796-817/Domain: transmembrane #status predicted <TM6>  
F;826-850/Domain: transmembrane #status predicted <TM7>  
F;104,233,403,525,757/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;636,699,961/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status pr  
F;705/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
F;892/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predi  
  
Query Match 16.8%; Score 821.5; DB 2; Length 1218;  
Best Local Similarity 25.6%; Pred. No. 7.6e-52;  
Matches 228; Conservative 182; Mismatches 372; Indels 109; Gaps 29;  
  
QY 53 LVIGGLPIDSRTIPANESILEPASAKC-----EGFNFORFRWKAMIHMIKEINKEKIDIL 108  
DB 51 IIGALFVSHHQ--PSTQV---AERKCEVREQGIQR---VEAMFHTLDRINSNPULL 102  
  
QY 109 PNITLGYQIFDFTCTISKSVAVLPLTQ-----QEENR-----PNFRNST 149  
DB 103 PNITLGCIRDSCHWSSVALEQSIFFIRDSLSIRDDNKOCTSRQWCIEGPPSPAT 162  
  
QY 150 GAPPAGIVGAGSFLSVSPASRILGLYLLPQVGYTSTCVILSKYQFPSPVLRVIADSKIQS 209  
DB 163 KRPIAGVIGPGSSVAIQVNLQLFNIPQIAYSATSIDLSKTLFKYPLRVVPSDTLQA 222  
  
QY 210 KAVVKRIQHFGWVWGAIAADDYGYKGVKTPKEMESANLCAVAFSETIPKYSN----- 264  
DB 223 RAILDIVKRYNNTYVSVAHTEGNYGSEAKPELASOGLCIAHSD---KIYSNAGEKH 279  
  
QY 265 -EKMOKAVKAVTSTAKVILVYTSIDLSLFLVLEMIHNIT-DRTWIATFAWITSALIAK 322  
DB 280 FDLRLKLRK-RLPKRVVVCCEGTVRGLMAMRRLGVAGEFLLIGSDGWADDEVVE 338  
  
QY 323 PBYFPYFGGTIGFATPRSVPLGKFLYDVHPNKPNDVLTIEFWQAFNCTWPNSSVY 382

Db	339	GYEQAVGG-ITVKLHSEEVTFDDYFLKRLNTNTRNPFQHRQCRIPGHPLF-	396
Qy	383	NVDRVNMWTKEDRLYDMSQOLCTGEBEKLBNKNTYDTSQRLITKQCOAVYIAHGLD	442
Db	397	NNYRKNN-----CSGVESLED---NVQDSKMGFV---INAIYAMAQGLH	435
Qy	443	--HLSRQEGOGPGSGNQCAIYPTDFWQLMYMYKEIKFK--SHEDKVVILDDNGDLKN	498
Db	436	DMHSHLCP-----GHVGLCKAMPIDGSQLLEFLMRTSTGVSGEDVW--FDENDTDP-	486
Qy	499	GRYDVLNHLHDEGEISFVTVGRFNFRSTNPFELVPTNFTNWTSSRLPHSVCTDVCP	558
Db	487	GRYEIMNLQYVEPCAFDYINVGSWHEGQLSID-----DYMQLINRSDWVLSVCSEPCS	539
Qy	559	PGTGRGVQVORPPICFPSIPICADGHVSRKPGECRCQCGEDYWSNAQKSECVLKEVEYLA	618
Db	540	KGEIKVIRKGEVSCCMWCTACKONEIVQ--DEFTCTACDLGMWPDPELGECEPITLRYLE	597
Qy	619	YDEALGFTLVLSVFGAFVVLAVTVVVIHRHTPLVNASDWQGLFIQVSLIIMLLSML	678
Db	598	WGNFESIVQVVFACGLGILVTSFVTFVLYRDTFVVKSSRELCLYILAGIFLYICPFT	657
Qy	679	FIDRPHNWSMAGQVTLALGFLSCLLGLKTSLSFLAYRISKSTQLTSMHPLY-----	733
Db	658	LIAQPTVASCYLQRLVGLSATMCSALVTKNR--IARILAGSKKKICTRKPFRMSAWA	715
Qy	734	RKIIVLISVLAIEIGICTAYLILEPMPVYKNWESQNTKIIILGCNEISIEFLYSNMGIDAF	793
Db	716	QLVIAGLVSVQLTLEVTIILEPMPVKSYPISR-EVFLICNTSTVG-WVAPLGYNGLL	773
Qy	794	ALLCPLTTFVARQLPDNYEGKCTTFGLMVFVFIWMSFVPLSTKGFQMAVEIFAILA	853
Db	774	IMSCYIYAFKTRNPANFNEAKYTAFTMYTTCIIWLAFVIYFGS--NYKIITTSFVSVL	831
Qy	854	SSHGLGCGIFAPKCLIIILLRPERN-----TSEIV-----CGRVSTTDNCI	893
Db	832	SVTVLGCWGFSPKIVILLAKPERNVSFAFTTSDVVRMHVGDGNVACRSNSL	882
RESULT 8			
JH0562			
Metabotropic glutamate receptor 3 precursor - rat			
C:Species: Rattus norvegicus (Norway rat)			
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004			
C:Accession: JH0562			
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigenoto, R.; Nakanishi, S.			
Neuron 8, 169-179, 1992			
A:Title: A family of metabotropic glutamate receptors.			
A:Reference number: JH0561; MUID:92110002; PMID:1309649			
A:Accession: JH0562			
A:Molecule type: mRNA			
A:Residues: 1-879 <TAN>			
A:Cross-references: UNIPROT:P31422			
A:Experimental source: brain			
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m			
C:Superfamily: metabotropic glutamate receptor 4			
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro			
F;1-22/Domain: signal sequence #status predicted <SIG>			
F;23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>			
F;577-599/Domain: transmembrane #status predicted <TRI>			
F;614-634/Domain: transmembrane #status predicted <TRI>			
F;646-664/Domain: transmembrane #status predicted <III>			
F;689-709/Domain: transmembrane #status predicted <TRV>			
F;735-756/Domain: transmembrane #status predicted <TRV>			
F;770-791/Domain: transmembrane #status predicted <TRV>			
F;804-828/Domain: transmembrane #status predicted <VII>			
F;209,292,414,439/Binding site: carboxylate (Asn) (covalent) #status predicted			
F;610,845/Binding site: phosphate (Ser) (covalent) #status predicted			

Query Match 16.6%; Score 814.5; DB 2; Length 879;  
 Best Local Similarity 26.6%; Pred. No. 1.6e-51;  
 Matches 240; Conservative 166; Mismatches 393; Indels 103; Gaps 30;

Qy	53	LVIGLGLPIDSKRTIPANESILEPASAKCEGFNFOR-FRWKAMIMHIKEIKRKOILPNI	111
Db	39	LVIGLGLFPIKEKGTCTEE-----CGRINEDRGIORLEAMLFAIDSKNDYLLPGV	89
Qy	112	TLGVOIFPTC-----FTISKSVAVLVUTGOENRPNFRNSTGAPP-----AGIVG	158
Db	90	KLGVHILDTCSRDYVLEQSLFVFRASLTQVDE--AEYMCDFGSAIOENIPLLIAGVIG	147
Qy	159	AGGSFLSPASRIILGLYLPQVGYTSTCVILSDYKQFFSYLSYASDIKQSKAVVVKIOH	218
Db	148	GSYSVSIVQANVLRLFLQIPQISYASTSAKLSKSDKRYDFARTVPPDFVQAKAMAILRF	207
Qy	219	FGWVWGAIAADDDYKGYKVTFFKEKMSANLCVAFSETIPKVIYSNEKMKAVK-AVKTS	277
Db	208	FNWTVSVIVASEGDYGETGIEAFQEAEARLNICIAAEKVGSRNIRKSYDSVIRELLQKP	267
Qy	278	TAKVIVLTSIDILSLFVLEMIHNITRWTATATWITSALIAK-PFPPFPFGGTIGFA	336
Db	268	NARVVVLFMRSD--SRELIAAANRVNASFTWASDGMGAQESIVKGEHVAY--GAITLE	324
Qy	337	TPRSVIPGLKFLYDVHKNKDPNDVLTTFEFTWATFNCTWPNSSVPYVNDHRVNMVTKEDR	396
Db	325	LASHVPRQDFYQSLNPNYNNHNPFRDFWEQKQCSLONKR-----NHR-----	370
Qy	397	LYDMSDQLCTGEBEKLKNTYDTSQRLITKQCOAVYIAHGLDHLR--COEGOGPF	454
Db	371	-----QVC--DKHLAIDSSNYEQESKIMFV--VNAVYAMAHALHKMORTLCP-----	413
Qy	455	GSNOQCAIPTDFWQL-MYMKKEIKF-----KSHEDKMWILDDNGDLKNGHYDVLNWH	507
Db	414	NTTKLCDAMKILDGKKLYKELKINFTAPFNPNKGADSIKVPDTFGD-GMGRYVFNQLQ	472
Qy	508	LDDEGEISVTVGRNFRSTNPFELVPTNTSTIFWNTSSRLPHSVCTDVCPGTGRGFVQ	567
Db	473	-QTGGKYSYLVKGVH-----AETLSLDVDSIHNSEN--VPTSQSDPCAPNEMKN-MQ	522
Qy	568	REPICFDSIPCADGHVSRKP-----GERECQCGEDYWSNAQKSECVLKEVEYLADEA	622
Db	523	PGDVCCWICIPC-----EPVEYLVDFTCMDCGPGQWPTADLSGCYNLPEDYIKWEDA	575
Qy	623	LGFTLVLSVFGAFVVLAVTVVVIHRHTPLVNASDWQGLFIQVSLIIMLLSMLFIDK	682
Db	576	WAGPVTIACLGFLCTCTIVITFIKHNTPLVKASRELICYILLFGVSLSYCMTFPIAK	635
Qy	683	PHNWSMAGQVTLALGFLSCLLGLKTSLSFLAYRISKSTQLT-S-MHPLYRKIIIVLIS	741
Db	636	PSPVICALRRLGLTGSFALCYSAALLTKNCIARI PDGVKNGAQRPKFISPSQVFCIGL	695
Qy	742	VLABIGICTAYLILEPMPV--YKNWESQNTKIIILGCNEISIEFLYSNMGIDAFLLCFL	799
Db	696	ILVQIVWVSVMILLETPTGTRRYTLPEKRET-VILKCNVKDSSMLISL-TYDVVVLIVICTV	753
Qy	800	TFVARQLPDNYEGKCTTFGLMVFPIIWMSPVPLSTKGFQMAVEIFAILASSHG--	857
Db	754	YAFKTRKCPENFENAEKFIQFTTTCIIWLAFPIFVTSDDRVQTTWCISVLSGFV	813
Qy	858	LLGCFIPAPKCLIIILLRPERNTSEIVCGRVSTTDNCIQLTSFAFVSSSELNNTVSTVLD	917
Db	814	VLGCLFAPKVIHVLFPQKN---VVTHRLHLNRFVSVSGTATTYSQSSASTVYVTCVNGRE	870
Qy	918	LI 919	
Db	871	VL 872	

RESULT 9

JC2132

metabotropic glutamate receptor 5 A - human

C:Species: Homo sapiens (man)  
 C>Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Jan-1996  
 C:Accession: JC2132  
 R:Minakami, R.; Katsumi, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.  
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994









```

QY 158 GAGSFLSPASRILGLYLPQVGYTSTCVILSDKYQPSYLRVIAADKIQSKAVKRIQ 217
Db 147 GPSSVAIQVQLQLFNIPQIAYASMDLSKTLFKYFMRVPSDAQARAVMDIVK 206
QY 218 HPGVWVGAIAADDDYGVKTKFKKMSANLCVAFSETIPKYSN---EKQKAVKAV 274
Db 207 RYNTVTSVHTSGTGESGMEAFKMSAKBGICIAHSY---KIYNSAGEQSFDKLKKL 263
QY 275 KT--STAKVILYTSIDISLFLVLEIHHNIT--DRTWIAEAW-----ITSALIAKPEYP 326
Db 264 RSHLPKRVAVACFCEGTVRGLLMAMRLGLAGEFLLGSDGWADYDVTG----- 315
QY 327 PYGGTIGFATPRSVIPGLK---EFLYDVHPKDPNDVITIEFWQAFNCTWPNSSVPYN 383
Db 316 -YOREAVGGITIKLOSPDKVDFDYLLKLRPETNLNPNWQFQWHRFQC----- 364
QY 384 VDRHVNTGKEDLYD--MSDQLCTGBEKLKNTYLDTSQRLITKQCKQAVYATAGL 441
Db 365 ---RLSGFAQENSKYKNTCNSSUTLTHVQDSKMGFV-----INALYSWAGL 410
QY 442 DH--LSRCQEGQPGFGSNOQCAIPTDFEWQLMYMYKEIKFKSHEDKWILDDNGDKNG 499
Db 411 HNMQSLCP-----GVAGLCDAMKPIDGRKLLDSLWKTFTGVSQDMILFDENG-SPG 463
QY 500 HYDVLNHLDDGEISFVTVGRNFRSTNPELVIPNSTIFWNTESSRLPHSVCTDVCP 559
Db 464 RYBIMNFKMGKDYFDYINVGSWD---NGELKWDDEV--W-SKKNNIIRSVCSBPCEK 516
QY 560 GTRGGRVQREPICFDSIPCADGHVSRKPCERCEOCGEDYNSNAQSKSVLKEVEYLAY 619
Db 517 GQIKVRKGVSQCTWCTPKENEYVF--DEYTKACQLGSGWPTDLDTCGDLIPQVLRW 574
QY 620 DEALGETVLVLSVFGAFVLAIVAVVTHRHRTPLVNASDWQLGFLQVSLIIMLSSMLF 679
Db 575 GDPEPTAAVFACLGLATLFTVTFIYDTPVKSSESLCYIILAGICGLYCTPCL 634
QY 680 IDKPHNSWCMAGQVTLALGSLCLLGTSSFLAYRISKTKQLTSMHPLY-----R 734
Db 635 IAKPKQIYCLVLRIGLSPMSYSALVTKTR--IARILAGSKKICTKPKRFSACAQ 692
QY 735 KIIVLSVLAEGICITAYLILEPMPVYKMSQNTKIIIGCNEISTEFLYSFGIDAFLA 794
Db 693 LVIAFLICIQGLIIVALEFMEPPDMDHYPSIR--EVLICNTNLG--VTPPLGVNGLLI 750
QY 795 LILCFLLTFVARQLPDNYEKGKCTFGMLVFFIWMSPVYLSLTKGKFMAVEIFAILAS 854
Db 751 LSTFTYAFKTRNVAPNPFNEAKYIAFTMYTTCIIWLAFVFIYFGS--NYKIIWCFVSLS 808
QY 855 SHGLGICFAPKCLIIILLRPN-----TSEIV 882
Db 809 ATVALGCMFVPKVYIILAKPERNVRSAGFTTSTVV 842

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## RESULT 13

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JH0561
metabotropic glutamate receptor 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0561
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Neuron 8, 169-179, 1992
A:Title: A family of metabotropic glutamate receptors.
A:Reference number: JH0561; MUID:921110002; PMID:1309649
A:Accession: JH0561
A:Molecule type: mRNA
A:Residues: 1-872 <TAN>
A:Cross-references: UNIPROT:P31421
C:Experimental source: brain
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by m
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

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F:568-590/Domain: transmembrane #status predicted <TRI>
F:605-625/Domain: transmembrane #status predicted <TII>
F:637-655/Domain: transmembrane #status predicted <III>
F:680-700/Domain: transmembrane #status predicted <TIV>
F:726-747/Domain: transmembrane #status predicted <TV>
F:761-782/Domain: transmembrane #status predicted <TVI>
F:795-819/Domain: transmembrane #status predicted <VII>
F:803-286,338,402,547/Binding site: carboxylate (Asn) (covalent) #status predicted
F:601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted
F:832/Binding site: phosphate (Thr) (covalent) #status predicted

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Query Match 15.6%; Score 764; DB 2; Length 872;
Best Local Similarity 25.3%; Pred. No. 8.1e-48;
Matches 240; Conservative 169; Mismatches 402; Indels 136; Gaps 31;

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QY 18 LAPLAELGSEAKKEBEERTCLLGKCKVADENHSLVIGGLPDPIDSRITPANESILEPAS 77
Db 10 LLLWG-----AVAGPAKKVUTLEG-----DLVLGLFPVHQGPABE----- 49
QY 78 AKCEGFNFQR--PRMKAMIMHIKEINRKRILNPITLGYQIFDTCTTISKSVEAVLFL- 135
Db 50 --CGPVNEHGGIQRLEAMLFALDRINRDPHLLPGVRLGAHILDSKOTHALEQALDFVR 107
QY 136 ----TGQENR---NFRNSTGA--FPAGIVGA--GGSP--LSVPASRIILGLYLPQVGYTS 184
Db 108 ASLSRGADGSRHICPDGSAVATHSDAPTAVTGVIGGSYSDVSQVANLLRLFOIPOISYAS 167
QY 185 TCVILSDKYQPSYLRVIAADDDYGVKTKFKKMSANLCVAFSETIPKYSN---EKQKAVK 244
Db 168 TSAKLSDKSRDYFARTVPPDPFQAKAMABILRFPNWTVTSTVASEGDTGETGIEAFELE 227
QY 245 MESANLCVAFSETIPKYSN---EKQKAVKA--VKTSTAKVILYTSIDISLFLVLEIHHNI 303
Db 228 ABARNICVATSEKVGSRAMRAFEVGRALLQKPSARVAVLFRSEDAELLAATQRLN- 286
QY 304 TDRTWIAEAW--ITGALIAKPEYFPFGTIGFATPRSVIPGLKFLYDVHPKDPNDVL 362
Db 287 ASFTVWASDGMGALSSVWAGSRAAEGAITIELAS--YPISDFASYFQSLDPWNNSRNPW 344
QY 363 TIEFWQTAFCNTWPN-----SSVPYVNVDRHVNTGKEDLYDMSDQLCTGBEKLDEL 414
Db 345 PFEFNEFPHCSFRORDCAHSLRAVPFEQBSKIMPV----- 381
QY 415 KNTYLDTSQRLITKQCKQAVYAIAGHLDHLSR--CQ-----EGQPGFSNOQCAIPTF 466
Db 382 -----VNAVYAWAHLENMHEALCPNTTHLCDAMPVNGRR----- 417
QY 467 DFWQLMY--YMKBIKF-----KSHEDKWILDDNGDLKNGHYDVILNHLDDSGEISFVTV 519
Db 418 ----LYKDFVLNVKFDAPFRPADTDDVRFDRFGD--GIGRYNIFTYLRAGSGRYRYQKV 471
QY 520 GRFNFRSTNPFELVIPNSTIFWNTESS--RLPHSVCTDVCPCPGTGRGVQREPICCFDSIP 578
Db 472 GYW-----ABGLTLDTSFIPWASPSAGPLPASRCSPECLQNEVKS--VQGEVCCWLCIP 524
QY 579 CADGHVSRKPCERCEOCGEDYNSNAQSKSVLKEVEYLAYDEALGFTLTVILSVFGAFVV 638
Db 525 CQP--VEYRLDEFTCADCGLYWPNASLTGCFELPQEIYRWGDMAWAGVPVTIACLGALAT 582
QY 639 LAVTAVYVTHRHRTPLVNASDWQLGFLQVSLIIMLSSMLFIDKPHNSWCMAGQVTLALG 698
Db 583 LFLVGLGVFVRHNATPVVKGASRELCYILLGGVPLCYCMTFVFIAKESTAVCTLRLRLGLTA 642
QY 699 RSLCLSLCLLGTSSFLAYRISKTKQLTS--MHPLYRKYIIVLSVLAEGICITAVLILRP 757
Db 643 FSVCSYALLTKTRNARIIFGGARSGAQRPFRFISASQVAICLALISGQLLIIVAAMLVREA 702
QY 758 PMVYKMSQNTKII--LGCNEISTEFLYSFGIDAFLALLCFELTTFVARQLPDNYEKGK 816
Db 703 PGTGETAPERREVVTLRCHNEDASMLGSL--AYNVLLIALCTLYAFKTKCKPENFEAKF 761
QY 817 ITFGMLVFFIHMSPVYLSLTKGKFMAVEIFAILASHG--LIGCTIPAPKCLIIILLRP 874

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Db 762 IGFTMYTTCIIWLAFLPIFYVTVSSDYRVQVTTMCVSVLSGSSVVLGCLFAPKLHILFQP 821

Qy 875 ERNTSEIVCGRVST--DNCIQITSAFVSSELNNTVSTVLDRLVLI 919

Db 822 QKN---VVSHPRAPTSRFGSAAPRASANLGQSGSQFVPTVCNGREV 865

RESULT 14

A49874

metabotropic glutamate receptor 7 - rat

N:Alternate names: metabotropic glutamate receptor mGluR7

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: A49874; 157954

R:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994

A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup

A:Reference number: A49874; MUID:94117433; PMID:8288595

A:Accession: A49874

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RES>

A:Cross-references: UNIPROT:P35400; GB:D16817; NID:g458728; PID:BAA04092.1; PID:g458729

R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994

A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid

A:Reference number: 157954; MUID:94195260; PMID:8145723

A:Accession: 157954

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-915 <RES>

A:Cross-references: EMBL:U06832; NID:g459657; PIDN:AAA20655.1; PID:g459658

C:Genetics:

A:Gene: mGluR7

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: neurotransmitter receptor

Query Match 15.5%; Score 758; DB 2; Length 915;

Best Local Similarity 24.3%; Pred. No. 2.4e-47; Indels 120; Gaps 32;

Matches 214; Conservative 191; Mismatches 354; Indels 120; Gaps 32;

Qy 53 LVIGGLFPIDRTIPANESILEPASAKCEGFNQR-FRNMKAMIMHIKEINKEKDIPLNI 111

Db 49 VTLGLLFPVHAK-----GPGGVPCGDIKRENGIHRLEAMLYALDQINSDPNLLPNV 99

Qy 112 TLGYQIFDPTCTISKSVEAVLFTLQ--ENRPNFRNSTGAPP-----AGIVCAGGS 162

Db 100 TLGARILDTCSRDTYALEQSLTFVQALIQKDTSDVRCNTEGPEPVFKPKVGVGICAGS 159

Qy 163 FLSPASRIILGLYLPQVGYTSTCVILSDKYQPSYLRVIASDKIOSKAVVKRIQHFGW 222

Db 160 SVSINMANILRLFQIPQISYASTAPELSDRRYDFSRVPPSPFQAQAVDIVKALGN 219

Qy 223 WVGAAADDDYGYGVKTFKE-KMESANLCAVFSETIPKYVSNKQKAV-----KAV 274

Db 220 YVSTLASGSGYKGVESFTQISKEAGGLCIAQSVRIQP-----ERKDTIDFRIIKQL 275

Qy 275 KISTAKVILVYTSIDLSLVF-----LEMIHNITDRTWIATWITSALIAKPEYFPYP 329

Db 276 DTPNSRAVVFANDEDIKQILAAAKRADQVGHFL-----WYGSDSW-GSKINPLHQHEDIA 330

Qy 330 GTTIGFATPRVPIQLKEFLYDHPNKDPNDVLITFEWQAFNCTWPNSSVPYVNDHRVN 389

Db 331 EGATIQKRAVTVGFDAYFTSRILENNRRNVWFAEYWEENFNC-----KLT 377

Qy 390 MTG--KEDRLYDMSDQLCTGEBKLEDLKNYTLDTSQLRITKQCKQAVYATAHGLHLR- 446

Db 378 LSGSKED-----TDRKCTGQERIGKDSN-YEQSGKQVQV---IDAVYMAHALHWNKD 428

Qy 447 -COEQCGFGNQCCAYIPTDFWQLMYMYKKEIKFKSHEDKWLDDNGDKNGHVDVLN 505

Db 429 LCADYRG-----VCPMEQAGGKKLLKYIRHNFNFGSAGTVPVNFNKGNDAP-GRYDIFQ 481

Qy 506 WHLDDGEISFVTVGRFNRSTNFELVPTNSTIIFWNTSESSRLPSVCTDVCPPGGRGF 565

Db 482 YQTTNTTTPGYRLIQW---TDELQLNI---EDMQKGVREIPSSVCTLPCKPGQ-RKK 534

Qy 566 VQREPIICFDSIPCADGHVSRKPGRECEQCEDYWSNAQKSECVLKVEYLYLAYDEALGF 625

Db 535 TOKGTPCCWTCEPC-DGY-QYQFDEMTQCHCPYDQRPENRTGCCQIPFIKLEWHSPWAV 592

Qy 626 TLVILSVFGAFVVLAVTVYVLRHTPLVNASDWGLFQLQVLSLIIMLSSMLFIDKPHN 685

Db 593 IPVFLAMIGIATIPVMTATFIRYNDTPIVRSGRELSYVLLTGIFCYIITFLMIKPDV 652

Qy 686 WSCMAGQVTLALGFLSCLSLGKTSLSFLAYRI-SKSKTQLTSMHPLRYKRIIVLSVLA 744

Db 653 AVCSEFRVFLGLGMCISYAALLTKNRI---YRIFEQKKSVTAPR-----LISPTS 701

Qy 745 EIGICTAYLI-----LEPMV-----YKNMESQNTKIILGNEISIEFLYSM 786

Db 702 QLAI-TSSLISVQLLGVFIWFGVDPENIIDIYDEHKTMPNEQARGVLRKCDITDLQICSL 760

Qy 787 FGIDAFALLCPLTTFVARQLPDNYEGKCIIFGMLVFFIIMSVFVPLYST-KGFKPMA 845

Db 761 -GYSILLMVTCTVYAIKTRGVDPENENAKPIGTMTTTCIVMLAFIPITFGTAQSAEKLY 819

Qy 846 VE---IFAILASSHGLLGCIPAPKCLIIILRPERNTSE 880

Db 820 IQTTTLTISMNLSASVALGMLYMPKYIIFHPELNVQK 858

RESULT 15

A46742

metabotropic glutamate receptor, mGluR6 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A46742

R:Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 268, 11868-11873, 1993

A:Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m

A:Reference number: A46742; MUID:93280152; PMID:8389366

A:Accession: A46742

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-871 <NAK>

A:Cross-references: UNIPROT:P35349; GB:D13963; NID:g391856; PIDN:BAA03066.1; PID:g391857

A:Experimental source: retina

A>Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBI:P.133250)

C:Superfamily: metabotropic glutamate receptor 4

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.8%; Score 724.5; DB 2; Length 871;

Best Local Similarity 24.9%; Pred. No. 6.4e-45;

Matches 217; Conservative 174; Mismatches 380; Indels 101; Gaps 28;

Qy 53 LVIGGLFPIDRTIPANESILEPASAKCEGF-NQFRNWKAMIMHIKEINKEKDIPLNI 111

Db 33 LTLGLLFPVHAR-----GAAGRACGALKKEQGVHRLEAMLYALDRVNDAPPELLPGV 83

Qy 112 TLGYQIFDPTCTISKSVEAVLFTLQEBNR-----PNFRNSTGAPPAGIV 157

Db 84 RLGARLLDTCSDRTYALEQSLFVQALIRGRGDDEASVRCGVPPLRSPAPERVAVV 143

Qy 158 GAGGSFLSPASRIILGLYLPQVGYTSTCVILSDKYQPSYLRVIASDKIOSKAVVKRIQ 217

Db 144 GASASSVSINMANVLRFLPAIPQISYASTAPELSDSTRYDFSRVPPSPFQAQAVDIVR 203

Qy 218 HFGWVWVGAIADDDYGYGVKTFKE-KMESANLCAVFSETIPKYVSNKQKAV-KAVK 275

Db 204 ALGWNVYVSTLASGSGYKGVESFTQISKEAGGLCIAQSVRIQIPREPFGFHKVIRLME 263

Qy 276 TSTAKVILVYTSIDLSLVFLEMIHNITDR-TWIAATEAW---ITSALIAKPEYFPYFGG 331

Db 264 TPNARGIILIFANEDDIRRVLEATROANLTGHFLWVGSDSWGSKISPLINLEEEAV---G 319



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